

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2005, 09:32:54 ; Search time 485 Seconds
(without alignments)
7799.412 Million cell updates/sec

Title: US-09-721-183-4
Perfect score: 639
Sequence: 1 ccgaacgaggttaggtcc.....cacgaatggacggaggggat 639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*
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2: Geneseqn19908.*
3: Geneseqn20009.*
4: Geneseqn20011.*
5: Geneseqn20013.*
6: Geneseqn20021.*
7: Geneseqn20023.*
8: Geneseqn20031.*
9: Geneseqn20033.*
10: Geneseqn20035.*
11: Geneseqn20037.*
12: Geneseqn20039.*
13: Geneseqn20041.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	639	100.0	639	5	AAD06846 Human bre
2	637.4	99.7	1104	8	ABZ71575 Breast sp
3	637.4	99.7	1104	12	ADP85817 Human bre
4	501.8	78.5	1011	4	AAK89498 Human dig
5	498.2	78.0	611	4	AAK87973 Human dig
6	350.4	54.8	2360	6	ABZ22025 Human NIP
7	306	47.9	307	8	ABZ71574 Breast sp
8	306	47.9	307	12	ADP85816 Human bre
9	99.8	15.6	766	10	ADC32261 Human nov
10	99.8	15.6	1192	10	ADC30390 Human nov
11	99.8	15.6	2112	10	ADB62991 Human cdn
12	75.8	11.9	503	11	ACN92793 Breast ca
13	45.2	7.1	202251	11	ACN44504 Mouse gen
14	42	6.6	53522	6	AD30228 Human PKD
15	42	6.6	53526	2	AAT94101 Human PKD
16	42	6.6	53577	2	AAT18551 Human pol
17	42	6.6	53577	2	AAT94108 Human PKD
18	39.2	6.1	540	13	ACN47094 Corton pr
19	38.4	6.0	2000	8	ADA71938 Rice gene
20	37.8	5.9	79640	13	ABD33007 Mouse can

21	37.4	5.9	1000	3	AAA02484	Aaa02484 Human col
22	37.4	5.9	118584	10	ADC87623	Adc87623 Human GPC
23	37.4	5.9	349999	10	ADC87010	Adc87010 Human GPC
24	37.2	5.8	1038	2	AAQ51019	Aaq51019 BBV VCA-p
25	37.2	5.8	172281	12	ADN12161	Adn12161 Epstein-B
26	36.6	5.7	10732	3	AAA10594	Aaa10594 Gene enco
27	36.2	5.7	203132	13	ABD33364	Abd33364 Murine ca
28	35.6	5.6	2230	11	ADM02845	Adm02845 Human cdn
29	35.6	5.6	7444	8	ABT19632	Abt19632 Aspergill
30	35.6	5.6	7496	8	ABT17818	Abt17818 Aspergill
31	35.6	5.6	8456	13	ADR84410	Adr84410 Aspergill
32	35.2	5.5	134442	13	ABD32824	Abd32824 Mouse can
33	35	5.5	1527	5	AAS68546	Aas68546 DNA enco
34	35	5.5	1620	5	AAS68547	Aas68547 DNA enco
35	35	5.5	2178	5	AAS86106	Aas86106 DNA enco
36	35	5.5	26047	11	ACN44246	Acn44246 Human gen
37	34.8	5.4	500	6	ABN15750	Abn15750 Human gen
38	34.8	5.4	500	13	ACN78840	Acn78840 Human GDM
39	34.8	5.4	505	12	ACH73908	Ach73908 Human gen
40	34.8	5.4	1967	4	AAI13118	Aai13118 Probe #30
41	34.8	5.4	1967	4	ABA54817	Abas4817 Human foe
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44	34.8	5.4	1967	4	ABA24581	Abas24581 Probe #30
45	34.8	5.4	1967	4	AAK28545	Aak28545 Human bon

ALIGNMENTS

RESULT 1
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ID AAD06846 standard; DNA; 639 BP.
XX
AC AAD06846;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human breast cancer specific gene-4 (BCSG-4).
XX
KW Human; breast cancer specific gene-4; BCSG-4; cytostatic; vaccine;
KW breast cancer; therapeutic; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200137779-A2.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US032056.
XX
PR 23-NOV-1999; 99US-0166973P.
XX
XX (DIAD-) DIADEXUS INC.
XX
PI Salceda S, Cafferkey R, Recipon H, Sun Y;
XX
DR WPI; 2001-367602/38.
XX
PT Novel breast cancer specific gene for diagnosing, monitoring, staging,
PT imaging, preventing and treating cancers, particularly breast cancer.
XX
PS Claim 1; Page 51; 66pp; English.
XX
CC The invention relates human breast cancer specific genes (BCSG's) and
CC their corresponding proteins. BCSG is useful for diagnosing, staging,
CC monitoring, imaging, preventing and treating breast cancers. BCSG is also
CC useful for inducing an immune response against a target cell expressing
CC BCSG. The invention also provide methods for detecting genetic lesions or
CC mutations in BCSG, thereby determining if a human with the genetic lesion
CC is at risk for breast cancer or has breast cancer. BCSG antibodies
CC labelled with paramagnetic ions or radioisotopes is useful for imaging
CC breast cancers, while BCSG antibodies conjugated to a cytotoxic agent is

PR 04-FEB-2000; 2000US-0180628P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-502630/55.
XX
XX Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognosing disorders of the
PT digestive system, particularly cancer and cancer metastases.
XX

```
PS Disclosure; SEQ ID NO 3074; 986pp; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a genomic DNA fragment
CC encoding a digestive system antigen of the invention
XX
SQ Sequence 1011 BP; 270 A; 220 C; 248 G; 273 T; 0 U; 0 Other;

Query Match      78.5%; Score 501.8; DB 4; Length 1011;
Best Local Similarity 99.6%; Pred. No. 4.4e-145;
Matches 503; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB |||||||
QY 61 TCCACCCCTCCACCTATGCCATGTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGAAAG 120
DB |||||||
QY 542 TCCACCCCTCCACCTATGCCATGTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGAAAG 601
DB |||||||
QY 121 CGAGGCTTAAGTAGTACGCTTCCCGACTTTGCTCAATGATAGCTGGGTCTAGC 180
DB |||||||
QY 602 GCAGGCTTAAGTAGTACGCTTCCCGACTTTGCTCAATGATAGCTGGGTCTAGC 661
DB |||||||
QY 181 TGGGTTCCAGCCACTTGAATGTGGGACATCTCTCACCCCAACTTTGTAGTGGAGCAAC 240
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QY 662 TGGGTTCCAGCCACTTGAATGTGGGACATCTCTCACCCCAACTTTGTAGTGGAGCAAC 721
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QY 782 CAGCAGGTAATCTGCTTCTAGCAAGTGGTGAAGTAAGAGAGCATCTGTATAGAGGCA 841
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QY 481 AGGTCAGGAGATTGCAGAGCAC 505
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RESULT 5
AAK87973
ID AAK87973 standard; cDNA; 611 BP.
XX
AC AAK87973;
XX
XX 05-NOV-2001 (first entry)
DE Human digestive system antigen coding sequence SEQ ID NO: 289.
DE
XX Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ss.
XX
OS Homo sapiens.
XX
XX WO200155314-A2.
PN
XX 02-AUG-2001.
XX
XX
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PF 17-JAN-2001; 2001WO-US001324.
XX
XX 31-JAN-2000; 2000US-0179065P.
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(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-502630/55.
P-PSDB; AAM92200.

PT Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognosing disorders of the
PT digestive system, particularly cancer and cancer metastases.
XX
PS Claim 1; SEQ ID NO 289; 986pp; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a cDNA encoding a digestive
CC system antigen of the invention
XX
SQ Sequence 611 BP; 133 A; 144 C; 153 G; 177 T; 0 U; 4 Other;
Query Match 78.0%; Score 498.2; DB 4; Length 611;
Best Local Similarity 98.6%; Pred. No. 4.5e-144;
Matches 555; Conservative 0; Mismatches 3; Indels 5; Gaps 5;
Qy 1 CCAGAACCGAGTTAGTCCAGGTTCTCGTTCTGGCAAATCTTTCTCTTACCTTCTTCC 60
Db 2 CCAGAACCGAGTTAGTCCAGGTTCTCGTTCTGGCAAATCTTTCTCTTACCTTCTTCC 61
Qy 61 TCCACCCCTCCACCTATGCCATGTTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGGAAAG 120
Db 62 TCCACCCCTCCACCTATGCCATGTTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGGAAAG 121
Qy 121 GCAGGCTTAAGTACCGTCTTCGGACCTTTGCTCAATGATAGCTGGGTGGTCTAGC 180
Db 122 GCAGGCTTAAGTACCGTCTTCGGACCTTTGCTCAATGATAGCTGGGTGGTCTAGC 181
Qy 181 TGGGTTCCAGCCACTTGTATGTGGGACATCTCTCACCCCAACTTTCTAGTGGAGCAAC 240
Db 182 TGGGTTCCAGCCACTTGTATGTGGGACATCTCTCACCCCAACTTTCTAGTGGAGCAAC 241
Qy 241 TGCTACAGAGGTAATATGATTAACCTTTACATTCATCTTTCTGCTCTCTCCAACTTAA 300
Db 242 TGCTACAGAGGTAATATGATTAACCTTTACATTCATCTTTCTGCTCTCTCCAACTTAA 301
Qy 301 CAGCAGGTAATCTGC-TTCTAGCAAGTGGTGAAGGTAAGAGAGCATCTGTATAGGAGGC 359
Db 302 CAGCAGGTAATCTGC-TTCTAGCAAGTGGTGAAGGTAAGAGAGCATCTGTATAGGAGGC 361
Qy 360 AAGAGATCTGAGTCTTTTGAAGGCCCTATCTCTGCTCTGCTCAATTAATCTTCTTC 419
Db 362 AAGAGATCTGAGTCTTTTGAAGGCCCTATCTCTGCTCTGCTCAATTAATCTTCTTC 421
Qy 420 ATTTCAATTATCTTACCTACTATTCAAGTTCCCTT-GATCTTTTCTTTGGGGCTGTC 478
Db 422 ATTTCAATTATCTTACCTACTATTCAAGTTCCCTTGGATCTTTCTTTGGGGCTGTC 481
Qy 479 TTAGGCTCAGGG-AGATTGAGAGACACAGAACTAGGAGGAGCCCTGA-GACATGGGGA 536
Db 482 TTAGGCTCAGGGTGGATTGAGAGACACAGAACTAGGAGGAGCCCTGAGGACATGGGGA 541
Qy 537 G-TTGGAGCTGAAGGAGGAATGG 558
Db 542 GTTTGGAGCTGAAGGAGGGAATTG 564
RESULT 6
ABZ22025
ID ABZ22025 standard; cDNA; 2360 BP.
XX
AC ABZ22025;
XX
DT 10-MAR-2003 (first entry)
XX Human NIP2 associated protein encoding cDNA SEQ ID NO:3.
DE
XX Human, nuclear cap binding protein interacting protein 2; NCBP; NIP2;
KW NCBP interacting protein; NIP2 associated protein; NIP2 AP; cancer; gene;
XX

KW Human; ss; gene; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease; cancer; tumour.

OS Homo sapiens.

FH Key Location/Qualifiers

FT 126..1199

FT /*tag= a

FT /product= "Clone PROST20063430 protein"

XX EP1308459-A2.

XX 07-MAY-2003.

XX 28-MAR-2002; 2002EP-00007401.

XX 05-NOV-2001; 2001JP-00379298.

PR 25-JAN-2002; 2002US-00350978.

XX (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S; Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Tamechika I; Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX WPI; 2003-450961/43.

DR P-PSDB; ADB64961.

XX New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.

XX Claim 1; Page; 222pp; English.

XX The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The polynucleotides and encoded proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours). The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a cDNA of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.

SQ Sequence 2112 BP; 497 A; 515 C; 573 G; 527 T; 0 U; 0 Other;

Query Match 15.6%; Score 99.8; DB 10; Length 2112;

Best Local Similarity 89.9%; Pred. No. 6.7e-20;

Matches 107; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 477 TCTTAGGTGAGGAGATTGCGAAGCAGCAGCACTAGGAGCAGCCCTGAGACATGGGA 536

DB 161 TGTGGGTGAGGAGATTGCGAAGCAGCAGCACTAGGAGCAGCCCTGAGACATGGGA 220

QY 537 GTTGAGCTGAAGGAGGAATGGCAGGATGAAGAAATCCCTAGGTGAGGACGTGTGAGG 595

Db 221 GTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAAATCCCTAGATTGCTTCTCTGAGGAGG 279

RESULT 12

ACN92793/c

ID ACN92793 standard; DNA; 503 BP.

XX ACN92793;

XX 02-DEC-2004 (first entry)

DE Breast cancer related marker, seq id 13943.

XX Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.

OS Homo sapiens.

XX US2003099974-A1.

XX 29-MAY-2003.

XX 18-JUL-2002; 2002US-00198846.

XX 18-JUL-2001; 2001US-0306220P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Lillie J, Xu Y, Wang Y, Steinmann K;

XX WPI; 2003-787014/74.

XX Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast cancer.

XX Disclosure; SEQ ID NO 13943; 36pp; English.

XX The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974

SQ Sequence 503 BP; 126 A; 134 C; 104 G; 134 T; 0 U; 5 Other;

Query Match 11.9%; Score 75.8; DB 11; Length 503;

Best Local Similarity 97.5%; Pred. No. 9.5e-13;

Matches 77; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 561 GGATGAAGAAATCCCTAGGTGAGGACGTGTGAGGGTGGTGGAAGGAGGGGTGCTC 620

DB 499 GGATGAAGAAATCCCTAGGTGAGGACGTGTGAGGGTGGTGGAAGGAGGGGTGCTC 440

QY 621 ACGAATGGACGAGGGGAT 639

DB 439 ACGAATGGACGAGGGGAT 421

RESULT 13

ACN44504

ID ACN44504 standard; DNA; 202251 BP.

XX ACN44504;

XX 18-NOV-2004 (first entry)

DE Mouse genomic sequence MCG20408.
XX Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
XX Mus musculus.
XX WO2003073826-A2.
XX PD 12-SEP-2003.
XX PF 28-FEB-2003; 2003WO-US006235.
XX PR 01-MAR-2002; 2002US-00087192.
XX PA (SAGR-) SAGRES DISCOVERY.
XX PI Morris DW;
XX WPI; 2003-328604/31.
XX PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
XX comprises a nucleotide sequence.
XX PS Claim 1; SEQ ID NO 985; Opp; English.
XX CC The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcino Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcino Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
XX SQ Sequence 202251 BP; 51742 A; 46659 C; 46432 G; 53759 T; 0 U; 3659 Other;
Query Match 7.1%; Score 45.2; DB 11; Length 202251;
Best Local Similarity 52.7%; Pred. No. 0.064;
Matches 98; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 452 CTGATCTTTTCTTCTTGGGGCTGCTTTAGGGTCAGGAGATTTCAGAGACACAGAAC 511
DB 140383 CCTGACATTGTGGACCTTGGGAGACAGAGATCACAGTACACAGCAGCAGCAGCAG 140442
QY 512 TAGGAGCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAAT 571
DB 140443 CAGCAGGAGAAAGAGAGAGAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 140502
QY 572 TCCCTAGGTAGGACGTGTAGGGTGGCTGGGAGAGGAGGGGTGGTCAAGATGGACG 631
DB 140503 AAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 140562
QY 632 GAGGGG 637
DB 140563 AAGAGG 140568
RESULT 14
AAD30228/c
ID AAD30228 standard; DNA; 53522 BP.
XX AC AAD30228;
XX DT 17-MAY-2002 (first entry)
XX DE Human PKD1 gene.
XX

KW Human; PKD1 gene; autosomal dominant polycystic kidney disease; ADPKD;
KW acquired cystic disease; transgenic animal; chromosome 16; ds.
XX Homo sapiens.
XX WO200206529-A2.
XX PD 24-JAN-2002.
XX PF 13-JUL-2001; 2001WO-US022035.
XX PR 13-JUL-2000; 2000US-0218261P.
XX PR 13-APR-2001; 2001US-0283691P.
XX PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX PI Germino GG, Watnick TJ, Phakdeekitcharoen B;
XX WPI; 2002-179805/23.
XX DR Novel primer for diagnosing polycystic kidney disease-associated
XX disorder, comprises regions having sequence that selectively hybridizes
XX to polycystic kidney disease gene sequence.
XX PS Claim 20; Page 127-156; 192pp; English.
XX CC The present invention relates to compositions and methods useful for the
CC identification and detection of polycystic kidney disease (PKD1) gene
CC mutations. The invention also relates to primers comprising a 5' region
CC having a sequence that selectively hybridizes to a PKD1 gene sequence and
CC optionally, to a PKD1 homologue sequence and an adjacent 3' region having
CC a sequence that selectively hybridizes to a PKD1 gene sequence and not to
CC a PKD1 homologue sequence. Primer pairs of the invention are useful for
CC detecting the presence or absence of a mutation in a PKD1 polynucleotide
CC in a sample, for identifying a subject at risk for a PKD1-associated
CC disorder such as autosomal dominant polycystic kidney disease (ADPKD) or
CC acquired cystic disease and for diagnosing a PKD1-associated disorder in
CC a subject. They are useful for selectively amplifying a region of a PKD1
CC gene. PKD1 DNA fragments are useful for detecting the presence of a mutant
CC PKD1 polynucleotide in a sample, as a probe for an amplification
CC reaction, in hybridisation or amplification assays of biological samples
CC to detect abnormalities of PKD1 expression and for engineering transgenic
CC animals. The present sequence is human PKD1 gene located on chromosome 16
XX SQ Sequence 53522 BP; 8486 A; 17664 C; 15766 G; 11606 T; 0 U; 0 Other;
Query Match 6.6%; Score 42; DB 6; Length 53522;
Best Local Similarity 52.9%; Pred. No. 0.32;
Matches 90; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY 469 GGGGGCTGTCTTAGGGTCAGGAGATTGCAGAAAGCAGAACCTAGGAGCAGCCCTGAGA 528
DB 34691 GCGGAGGGGAGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 34632
QY 529 CATGGGAGTTGGAGCTCAAGAGGAGGAGTGGCAGGATGAAGATTCCCTAGGTAGGACCT 588
DB 34631 GAGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 34572
QY 589 GTGAGGGTGGCTGGGAGAAAGGGGGTGGTTCACGAATGGAGGGGGA 638
DB 34571 GAGGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 34522
RESULT 15
AAT94101/c
ID AAT94101 standard; DNA; 53526 BP.
XX AC AAT94101;
XX DT 25-MAR-2003 (revised)
XX DT 01-JUN-1998 (first entry)
XX DE Human PKD1 gene.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2005, 09:32:49 ; Search time 168 Seconds
(without alignments)
6223.695 Million cell updates/sec

Title: US-09-721-183-4

Perfect score: 639

Sequence: 1 ccagacgagtgtagtcc.....cacgaatggacggggggat 639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
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4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	45.2	7.1	7218	1	US-08-232-463-14
C 2	42	6.6	53526	3	US-08-658-136-2
C 3	42	6.6	53577	3	US-08-658-136-1
C 4	39.8	6.2	7218	1	US-08-232-463-14
C 5	38.2	6.0	8279	4	US-09-949-016-13478
C 6	37.2	5.8	1038	1	US-08-031-148-3
C 7	37.2	5.8	1038	3	US-08-415-838-3
C 8	37.2	5.8	1038	3	US-09-205-169-3
C 9	36.4	5.7	79350	4	US-09-949-016-12467
C 10	36.4	5.7	79351	4	US-09-949-016-16275
C 11	36.4	5.7	247781	4	US-09-949-016-14193
C 12	36.2	5.7	149971	4	US-09-949-016-13590
C 13	36	5.6	462	4	US-09-621-976-15621
C 14	35.4	5.5	120727	4	US-09-949-016-15787
C 15	35.4	5.5	120727	4	US-09-949-016-15788
C 16	35.2	5.5	18955	4	US-09-949-016-13343
C 17	35.2	5.5	30678	4	US-09-949-016-12818
C 18	34.8	5.4	500	4	US-09-866-108A-15742
C 19	34.8	5.4	1141	4	US-09-806-708B-22
C 20	34.8	5.4	231129	4	US-09-949-016-16110
C 21	34.8	5.4	262993	4	US-09-949-016-11934
C 22	34.6	5.4	9052	4	US-09-949-016-13662
C 23	34.6	5.4	23802	4	US-09-949-016-12107
C 24	34.6	5.4	23803	4	US-09-949-016-15878
C 25	34.6	5.4	174029	4	US-09-949-016-12610
C 26	34.6	5.4	174030	4	US-09-949-016-13880
C 27	34.4	5.4	289	3	US-09-007-005-17

28	34.4	5.4	289	3	US-09-244-796-17	Sequence 17, Appl
29	34.4	5.4	3614	4	US-09-221-013A-9	Sequence 9, Appl
30	34.2	5.4	601	4	US-09-949-016-103065	Sequence 103065,
31	34.2	5.4	601	4	US-09-949-016-103140	Sequence 103140,
32	34.2	5.4	601	4	US-09-949-016-187952	Sequence 187952,
33	34.2	5.4	15907	4	US-09-949-016-16818	Sequence 16818, A
34	34.2	5.4	300598	4	US-09-949-016-11868	Sequence 11868, A
35	34.2	5.4	302604	4	US-09-949-016-14588	Sequence 14588, A
36	34.2	5.4	302604	4	US-09-949-016-14589	Sequence 14589, A
37	34.2	5.4	308362	4	US-09-949-016-17119	Sequence 17119, A
38	34	5.3	6585	4	US-09-949-016-14470	Sequence 14470, A
C 39	33.8	5.3	3293	4	US-09-949-016-4658	Sequence 4658, App
C 40	33.8	5.3	3314	4	US-09-949-016-836	Sequence 836, App
C 41	33.8	5.3	4544	4	US-08-956-171E-517	Sequence 517, App
C 42	33.8	5.3	4544	4	US-08-781-986A-517	Sequence 517, App
C 43	33.8	5.3	31440	4	US-09-949-016-12578	Sequence 12578, A
C 44	33.8	5.3	31444	4	US-09-949-016-16400	Sequence 16400, A
C 45	33.8	5.3	78649	4	US-09-949-016-14619	Sequence 14619, A

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, P.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESS: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14

Query Match 7.1%; Score 45.2; DB 1; Length 7218;


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; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935.313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F18
;
US-08-232-463-14
Query Match 6.2%; Score 39.8; DB 1; Length 7218;
Best Local Similarity 5.4%; Pred. No. 0.12;
Matches 17; Conservative 167; Mismatches 129; Indels 0; Gaps 0;

Qy 7 CCGAGTTTAGTCCAGGTTCTCGTTCTGGCAAATCTTCTCTACCTTCTTCTCCACC 66
Db 1033 CCGAGTTTAGTCCAGGTTCTCGTTCTGGCAAATCTTCTCTACCTTCTTCTCCACC 66
Qy 67 CCTCACCTATGCCATGTTTCCCTTACCCACTCCAGCTCGGTGGAGGAAGCAGGC 126
Db 1093 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1152
Qy 127 CTAAGTAGTACCGCTCTCCGACCTTGTCTCAATGATAGCTGGGTGGGTCTAGCTGGGTT 186
Db 1153 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1212
Qy 187 CCAGCCACTTGAATGTGGGACATCTCTCACCCCAACTTTGTAGGTGAGCAACTGTAC 246
Db 1213 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1272
Qy 247 AGAGTAATATGATTAATCTTACATTCATCTTCTGCTGCTCCCAACTTAACAGAG 306
Db 1273 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1332
Qy 307 GTAATCTGCTTCT 319
Db 1333 YYYYYYYYYYYY 1345

RESULT 5
US-09-949-016-13478
; Sequence 13478, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13478
; LENGTH: 8279
; TYPE: DNA
; ORGANISM: Human
;
US-09-949-016-13478
Query Match 6.0%; Score 38.2; DB 4; Length 8279;
Best Local Similarity 52.1%; Pred. No. 0.42;
Matches 85; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 469 GGGGGCTGCTTCTAGGTCAGGAGATTCCAGAAGCACCAGAACTAGGAGCAGCCCTGACA 528
Db 1215 GGGGGCATAGGTGTGGAAGGGGTGGGGAAGAGGGGCCAGGAGTGGGGTGGAAGAGGGG 1274
Qy 529 CATGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAAATTCCTTAGGTGAGGACGT 588
Db 1275 AAAGAAGAGGATAGGAGGACAGGACAGGAGAGGCCAGGATGGGTAGGAGGGAAGA 1334
Qy 589 GTGAGGTGGCTGGGAGAAAGGGAGGGGTGGTCACGAATGGAGC 631
Db 1335 CAGAGGAGGGGGGACGAGGGGGCGGATGAAGAGGGGGCG 1377

RESULT 6
US-08-031-148-3/c
; Sequence 3, Application US/08031148
; Patent No. 5424398
; GENERAL INFORMATION:
; APPLICANT: Middelorp, Jaap Michiel..
; TITLE OF INVENTION: Peptides and nucleic acid sequences
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo Pharma
; STREET: 1330-A Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850-4377
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/031.148
; FILING DATE: 19930312
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92200721.6
; FILING DATE: 13-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bobrowicz, Donna

```

```

; REGISTRATION NUMBER: 32,196
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1038 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Epstein-Barr virus
;
US-08-031-148-3

Query Match          5.8%; Score 37.2; DB 1; Length 1038;
Best Local Similarity 52.6%; Pred. No. 0.27;
Matches 81; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 457 TCCTTTCTTCTTGGGGCTGTCTTAGGGTCAGGAGATTGCAGAAGCACCAGAACTAGGA 516
Db 468 TCCTTTCCGCTTGTGGATCCGAGGAGCGGGGACGTAGTCTGCCCGCAAGTGGGATCC 409
Qy 517 GCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGAGGAATGGCAGGATGAAGAATTCCT 576
Db 408 GTAGTAAGGAGGACGCGGTGGAGGGGCCAAAGAGCCCGCAAGTAGGCGG 349
Qy 577 AGGTGAGGACGTGTGAGGGTGGCTGGGAGAGGG 610
Db 348 AGGGGGTGTGGTGGGGTGGTAGGTGTGAGCG 315

RESULT 8
US-09-205-169-3/c
; Sequence 3, Application US/09205169
; Patent No. 6365717
; GENERAL INFORMATION:
; APPLICANT: Middeldorp, Jaap Michiel.
; TITLE OF INVENTION: Peptides and nucleic acid sequences
; related to the Epstein-Barr virus.
;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo-No. 6365717el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/205,169
; FILING DATE: 04-Dec-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/415,838
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1038 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Epstein-Barr virus
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-205-169-3

Query Match          5.8%; Score 37.2; DB 3; Length 1038;
Best Local Similarity 52.6%; Pred. No. 0.27;
Matches 81; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 457 TCCTTTCTTCTTGGGGCTGTCTTAGGGTCAGGAGATTGCAGAAGCACCAGAACTAGGA 516
Db 468 TCCTTTCCGCTTGTGGATCCGAGGAGCGGGGACGTAGTCTGCCCGCAAGTGGGATCC 409
Qy 517 GCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGAGGAATGGCAGGATGAAGAATTCCT 576
Db 408 GTAGTAAGGAGGACGCGGTGGAGGGGCCAAAGAGCCCGCAAGTAGGCGG 349
Qy 577 AGGTGAGGACGTGTGAGGGTGGCTGGGAGAGGG 610
Db 348 AGGGGGTGTGGTGGGGTGGTAGGTGTGAGCG 315

US-08-838-3/c
; Sequence 3, Application US/08415838
; Patent No. 6008327
; GENERAL INFORMATION:
; APPLICANT: Middeldorp, Jaap Michiel.
; TITLE OF INVENTION: Peptides and nucleic acid sequences
; related to the Epstein-Barr virus.
;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo-No. 6008327el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,838
; FILING DATE: 03-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92200721.6
; FILING DATE: 13-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1038 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Epstein-Barr virus
;
US-08-415-838-3

Query Match          5.8%; Score 37.2; DB 3; Length 1038;
Best Local Similarity 52.6%; Pred. No. 0.27;
Matches 81; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 457 TCCTTTCTTCTTGGGGCTGTCTTAGGGTCAGGAGATTGCAGAAGCACCAGAACTAGGA 516
Db 468 TCCTTTCCGCTTGTGGATCCGAGGAGCGGGGACGTAGTCTGCCCGCAAGTGGGATCC 409
Qy 517 GCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGAGGAATGGCAGGATGAAGAATTCCT 576
Db 408 GTAGTAAGGAGGACGCGGTGGAGGGGCCAAAGAGCCCGCAAGTAGGCGG 349
Qy 577 AGGTGAGGACGTGTGAGGGTGGCTGGGAGAGGG 610
Db 348 AGGGGGTGTGGTGGGGTGGTAGGTGTGAGCG 315

US-08-838-3/c
; Sequence 3, Application US/08415838
; Patent No. 6008327
; GENERAL INFORMATION:
; APPLICANT: Middeldorp, Jaap Michiel.
; TITLE OF INVENTION: Peptides and nucleic acid sequences
; related to the Epstein-Barr virus.
;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo-No. 6008327el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,838
; FILING DATE: 03-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92200721.6
; FILING DATE: 13-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1038 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Epstein-Barr virus
;
US-08-415-838-3

Query Match          5.8%; Score 37.2; DB 3; Length 1038;
Best Local Similarity 52.6%; Pred. No. 0.27;
Matches 81; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
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RESULT 9

US-09-949-016-12467/c
; Sequence 12467, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12467
; LENGTH: 79350
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(79350)
; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12467

Query Match 5.7%; Score 36.4; DB 4; Length 79350;
Best Local Similarity 55.6%; Pred. No. 5.6;
Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 351 ATAGGAGCAAGAGATCGAGTCCTTTTGAAGGCTATCCCTGCTGTCGTATCTCAATTA 410
Db 65064 AAAGGAACAGAGAGATGTCAGAGAGAGAGAGATGTCGTGCTCTCTCTCTCT 65005

Qy 411 CTGTTCTTCATTTCAATTTATCTTACCTACTATTCAAGTTCCTTGTATCTTTCTTTGG 470
Db 65004 CTCTCTTCATTTCTCTTATTTGTTAACTCATTTTCAGCTCCTTTGGGTTTCACITTTGGA 64945

Qy 471 GGGCTG 476
Db 64944 GCACTG 64939

RESULT 10

US-09-949-016-16275/c
; Sequence 16275, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16275
; LENGTH: 79351
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(79351)
; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-16275

Query Match 5.7%; Score 36.4; DB 4; Length 79351;
Best Local Similarity 55.6%; Pred. No. 5.6;
Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 351 ATAGGAGCAAGAGATCGAGTCCTTTTGAAGGCTATCCCTGCTGTCGTATCTCAATTA 410
Db 65064 AAAGGAACAGAGAGATGTCAGAGAGAGAGAGATGTCGTGCTCTCTCTCTCTCT 65005

Qy 411 CTGTTCTTCATTTCAATTTATCTTACCTACTATTCAAGTTCCTTGTATCTTTCTTTGG 470
Db 65004 CTCTCTTCATTTCTCTTATTTGTTAACTCATTTTCAGCTCCTTTGGGTTTCACITTTGGA 64945

Qy 471 GGGCTG 476
Db 64944 GCACTG 64939

RESULT 11

US-09-949-016-14193/c
; Sequence 14193, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14193
; LENGTH: 247781
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(247781)
; OTHER INFORMATION: n = A,T,C or G

Query Match

5.7%; Score 36.4; DB 4; Length 247781;
Best Local Similarity 51.9%; Pred. No. 11;
Matches 82; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 481 AGGCTCAGGAGATTGTCAGAGAGACCAAGAACTAGGAGCAGCCCTGAGACATGGGAGTTG 540
Db 126708 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 126649

Qy 541 GAGCTGAAGGAGGAATGCGAGGATGAAGAAATTCCTAGGTGAGGACGCTGTGAGGGTGGCT 600
Db 126648 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 126589

Qy 601 GGGAGAAGGAGGGGTGCTACGAATGGACCGAGGGGA 638
Db 126588 GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 126551

RESULT 12

US-09-949-016-13590
; Sequence 13590, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF


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Query Match      5.5%; Score 35.4; DB 4; Length 120727;
Best Local Similarity 57.8%; Pred. No. 15;
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy      80 CATGTTTCCCTTAGCCACTCCAGCTCGGTGAGGAAAGCGAGCCCTAACTAGGTACC 139
Db      17139 CAGCCTTTTGTCTCAGCTGCTCTCTGGTTCTGTGTCGAGAGGGAGGCCAGTGAGGATGC 17198

Qy      140 GTCTTCCCGACTTTTGCTCAATGATAGCTGGGTGGGTCTAGCTGGGTTCC 188
Db      17199 GTTTCGGGGAGTTTGCAGACTGCTAGCGAGGCTGCCTAACCGAGTGCC 17247
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Search completed: October 12, 2005, 09:35:50
Job time : 172 secs

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SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	637.4	99.7	1104	16	US-10-082-828A-35	Sequence 35, Appl
2	637.4	99.7	1104	24	US-11-057-807-35	Sequence 35, Appl
3	306	47.9	307	15	US-10-082-828A-34	Sequence 34, Appl
4	306	47.9	307	24	US-11-057-807-34	Sequence 34, Appl
5	99.8	15.6	2112	17	US-10-104-047-1145	Sequence 1145, Ap
c	75.8	11.9	503	14	US-10-198-846-13943	Sequence 13943, A
6	71	7.1	202251	13	US-10-087-192-985	Sequence 985, App
7	45.2	7.1	202251	13	US-10-087-192-985	Sequence 985, App

C	8	42	6.6	53523	10	US-09-504-968A-1	Sequence 1, Appl
		6.1	540	19	US-10-021-323-1875	Sequence 1875, Ap	
C	10	39.2	6.1	540	13	US-10-027-632-236295	Sequence 236295,
		37.4	5.9	610	13	US-10-027-632-236296	Sequence 236296,
C	11	37.4	5.9	610	13	US-10-027-632-236297	Sequence 236297,
		37.4	5.9	610	13	US-10-027-632-236298	Sequence 236298,
C	13	37.4	5.9	610	13	US-10-027-632-236299	Sequence 236299,
		37.4	5.9	610	17	US-10-027-632-236295	Sequence 236295,
C	15	37.4	5.9	610	17	US-10-027-632-236296	Sequence 236296,
		37.4	5.9	610	17	US-10-027-632-236297	Sequence 236297,
C	17	37.4	5.9	610	17	US-10-027-632-236298	Sequence 236298,
		37.4	5.9	610	17	US-10-027-632-236299	Sequence 236299,
C	18	37.4	5.9	610	17	US-10-027-632-236298	Sequence 236298,
		37.4	5.9	610	17	US-10-027-632-236299	Sequence 236299,
C	20	37.4	5.9	394468	21	US-10-741-600-17952	Sequence 17952, A
		37.4	5.9	418550	17	US-10-741-600-17952	Sequence 17952, A
C	21	37.4	5.9	418550	17	US-10-741-600-17952	Sequence 17952, A
		37.2	5.8	451	18	US-10-741-600-17952	Sequence 17952, A
C	22	37.2	5.8	451	18	US-10-741-600-17952	Sequence 17952, A
		37.2	5.8	1038	13	US-10-424-599-138280	Sequence 138280,
C	23	37.2	5.8	1038	13	US-10-424-599-138280	Sequence 138280,
		37.2	5.8	2839	18	US-10-425-114-32733	Sequence 3, Appli
C	24	37.2	5.8	2839	18	US-10-425-114-32733	Sequence 32733, A
		37.2	5.8	3134	20	US-10-425-115-119600	Sequence 119600,
C	25	36.6	5.7	195	19	US-10-437-963-20090	Sequence 20090, A
		36.6	5.7	195	19	US-10-437-963-20090	Sequence 20090, A
C	27	36.6	5.7	976	19	US-10-437-963-8451	Sequence 8451, Ap
		36.2	5.7	11263	22	US-10-756-149-3787	Sequence 3787, Ap
C	28	36.2	5.7	11263	22	US-10-756-149-3787	Sequence 3787, Ap
		36.2	5.7	203132	19	US-10-322-281-459	Sequence 459, App
C	29	36.2	5.7	203132	19	US-10-322-281-459	Sequence 459, App
		36	5.6	1599	18	US-10-425-114-33012	Sequence 33012, A
C	30	36	5.6	1599	18	US-10-425-114-33012	Sequence 33012, A
		31	5.6	1599	20	US-10-425-115-141198	Sequence 141198,
C	32	35.8	5.6	592	13	US-10-027-632-280778	Sequence 280778,
		33	5.6	592	13	US-10-027-632-280778	Sequence 280778,
C	33	35.8	5.6	592	13	US-10-027-632-280778	Sequence 280778,
		34	5.6	735	13	US-10-027-632-26656	Sequence 26656, A
C	34	35.8	5.6	735	13	US-10-027-632-26656	Sequence 26656, A
		35	5.6	735	17	US-10-027-632-26656	Sequence 26656, A
C	35	35.8	5.6	735	17	US-10-027-632-26656	Sequence 26656, A
		35.8	5.6	401433	22	US-10-737-082-79	Sequence 79, Appl
C	36	35.8	5.6	401433	22	US-10-737-082-79	Sequence 79, Appl
		37	5.6	401433	22	US-10-765-790-15	Sequence 124398,
C	37	35.8	5.6	608	20	US-10-425-115-124398	Sequence 124398,
		38	5.6	608	20	US-10-425-115-124398	Sequence 124398,
C	38	35.6	5.6	2230	30	US-10-108-260A-1530	Sequence 1530, Ap
		35	5.6	7444	15	US-10-128-714-5176	Sequence 5176, Ap
C	40	35.6	5.6	7444	15	US-10-128-714-5176	Sequence 5176, Ap
		41	5.6	7496	15	US-10-128-714-176	

ALIGNMENTS

RESULT 1

US-10-082-828A-35
; Sequence 35, Application US/10082828A

; Publication No. US20030175715A1

APPLICANT: SUN. YONG

APPLICANT: Recipon, Herve

; APPLICANT: Salceda, Susana

APPLICANT: Liu, Chenghua

APPLICANT: Turner Leah

; TITLE OF INVENTION: Composition

FILE REFERENCE: DEX-0247

CURRENT APPLICATION NUMBER: 2002-
CURRENT FILING DATE: 2002-

;; CURRENT FILING DATE: 2002
;; PRIOR APPLICATION NUMBER: U

; PRIOR FILING DATE: 2000-10-

; NUMBER OF SEQ ID NOS: 266

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; SOFTWARE: PACENCIII VERSION
; SEQ ID NO 35

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; LENGTH: 1104

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; TYPE: DNA

ORGANISM: HOMO SAPIENS
ISS-10-082-828A-35

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0
2
5
4
0
4
0
0
2
4
0
0

Query Match

Best Local Similarity 99.8
Matches 638. Conservative

DATE RECEIVED, 1960 JAN 11

Qy 1 CCAGAACCGAGTTTAC

Dd	466	CCAGAACGAGTTTAGTCCAGGTTCTCGTTCTGGCAAAATCTTCTCCTTACCTTCTTCC	525
Qy	61	TCCACCCCTCCACCTATGCCATGTTTTCCTTACCACTCCCGAGCTCGGTGGAGGAAAG	120
Dd	526	TCCACCCCTCCACCTATGCCATGTTTTCCTTACCACTCCCGAGCTCGGTGGAGGAAAG	585
Qy	121	GCAGGCCCTAACTAGTAGTACCGTCTTCCGACATTTGCTCAATGATAGCTGGGTGGGTCTAGC	180
Dd	586	GCAGGCCCTAACTAGTAGTACCGTCTTCCGACATTTGCTCAATGATAGCTGGGTGGGTCTAGC	645
Qy	181	TGGGTTCCAGGCACCTGTAATGTGGGACATCTCCACCCCACTTTGTAGGTGAGCAAC	240
Dd	646	TGGGTTCCAGGCACCTGTAATGTGGGACATCTCCACCCCACTTTGTAGGTGAGCAAC	705
Qy	241	TGCTACAGAGGTAATAATGATTAATCTTACATTTCCATCTTTCGTCCTGCCAACTTAA	300
Dd	706	TGCTACAGAGGTAATAATGATTAATCTTACATTTCCATCTTTCGTCCTGCCAACTTAA	765
Qy	301	CAGCAGGTAATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAGCATCTGTATAGGAGGCA	360
Dd	766	CAGCAGGTAATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAGCATCTGTATAGGAGGCA	825
Qy	361	AGAGATCTGAGTCTTTTGAAGGCTATCTCTGCTCTGTATCTCAATTTACTGTTCTTCA	420
Dd	826	AGAGATCTGAGTCTTTTGAAGGCTATCTCTGCTCTGTATCTCAATTTACTGTTCTTCA	885
Qy	421	TTTCAATTTACTTACTACTATTCAGTTCCTTGTATCTTCTTCTTGGGGCTGCTT	480
Dd	886	TTTCAATTTACTTACTACTATTCAGTTCCTTGTATCTTCTTCTTGGGGCTGCTT	945
Qy	481	AGGTCAGGGAGATTGCAAGACCCAGAACTAGGAGCAGCCCTGAGACATGGGGAGTTG	540
Dd	946	AGGTCAGGGAGATTGCAAGACCCAGAACTAGGAGCAGCCCTGAGACATGGGGAGTTG	1005
Qy	541	GAGTCAGAGGAGGATGGCAGGATGAAGATTCCTTAGTGAGGACGTGTGAGGGTGGCT	600
Dd	1006	GAGTCAGAGGAGGATGGCAGGATGAAGATTCCTTAGTGAGGACGTGTGAGGGTGGCT	1065
Qy	601	GGGAGAGGGAGGGGTGCTACGAAATGGACGGAGGGAT	639
Dd	1066	GGGAGAGGGAGGGGTGCTACGAAATGGACGGAGGGAT	1104
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US-11-057-807-35			
; Sequence 35, Application US/11057807			
; Publication No. US20050136473A1			
; GENERAL INFORMATION:			
; APPLICANT: Sun, Yongming			
; APPLICANT: Recipon, Herve			
; APPLICANT: Salceda, Susana			
; APPLICANT: Liu, Chenghua			
; APPLICANT: Turnez, Leah			
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr			
; FILE REFERENCE: DEX-0247			
; CURRENT APPLICATION NUMBER: US/11/057,807			
; PRIOR FILING DATE: 2005-02-14			
; PRIOR APPLICATION NUMBER: US/10/082,828			
; PRIOR FILING DATE: 2002-07-09			
; PRIOR APPLICATION NUMBER: US 60/243,805			
; PRIOR FILING DATE: 2000-10-27			
; NUMBER OF SEQ ID NOS: 266			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 35			
; TYPE: DNA			
; LENGTH: 1104			
; ORGANISM: Homo sapiens			
US-11-057-807-35			
Query Match 99.7%; Score 637.4; DB 24; Length 1104;			
Best Local Similarity 99.8%; Pred. No. 2.4e-194;			
Matches 638; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			

Qy	1	CCAGAACCGAGTTTAGTCCAGGTTCTCGTTCTGGCAAAATCTTCTCCTTACCTTCTTCC	60
Dd	466	CCAGAACCGAGTTTAGTCCAGGTTCTCGTTCTGGCAAAATCTTCTCCTTACCTTCTTCC	525
Qy	61	TCCACCCCTCCACCTATGCCATGTTTTCCTTACCACTCCCGAGCTCGGTGGAGGAAAG	120
Dd	526	TCCACCCCTCCACCTATGCCATGTTTTCCTTACCACTCCCGAGCTCGGTGGAGGAAAG	585
Qy	121	GCAGGCCCTAACTAGTAGTACCGTCTTCCGACATTTGCTCAATGATAGCTGGGTGGGTCTAGC	180
Dd	586	GCAGGCCCTAACTAGTAGTACCGTCTTCCGACATTTGCTCAATGATAGCTGGGTGGGTCTAGC	645
Qy	181	TGGGTTCCAGGCACCTGTAATGTGGGACATCTCTCACCCCACTTTGTAGGTGAGCAAC	240
Dd	646	TGGGTTCCAGGCACCTGTAATGTGGGACATCTCTCACCCCACTTTGTAGGTGAGCAAC	705
Qy	241	TGCTACAGAGGTAATAATGATTAATCTTACATTTCCATCTTTCGTCCTGCCAACTTAA	300
Dd	706	TGCTACAGAGGTAATAATGATTAATCTTACATTTCCATCTTTCGTCCTGCCAACTTAA	765
Qy	301	CAGCAGGTAATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAGCATCTGTATAGGAGGCA	360
Dd	766	CAGCAGGTAATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAGCATCTGTATAGGAGGCA	825
Qy	361	AGAGATCTGAGTCTTTTGAAGGCTATCTCTGCTCTGTATCTCAATTTACTGTTCTTCA	420
Dd	826	AGAGATCTGAGTCTTTTGAAGGCTATCTCTGCTCTGTATCTCAATTTACTGTTCTTCA	885
Qy	421	TTTCAATTTACTTACTACTATTCAGTTCCTTGTATCTTCTTCTTGGGGCTGCTT	480
Dd	886	TTTCAATTTACTTACTACTATTCAGTTCCTTGTATCTTCTTCTTGGGGCTGCTT	945
Qy	481	AGGTCAGGGAGATTGCAAGACCCAGAACTAGGAGCAGCCCTGAGACATGGGGAGTTG	540
Dd	946	AGGTCAGGGAGATTGCAAGACCCAGAACTAGGAGCAGCCCTGAGACATGGGGAGTTG	1005
Qy	541	GAGTCAGAGGAGGATGGCAGGATGAAGATTCCTTAGTGAGGACGTGTGAGGGTGGCT	600
Dd	1006	GAGTCAGAGGAGGATGGCAGGATGAAGATTCCTTAGTGAGGACGTGTGAGGGTGGCT	1065
Qy	601	GGGAGAGGGAGGGGTGCTACGAAATGGACGGAGGGAT	639
Dd	1066	GGGAGAGGGAGGGGTGCTACGAAATGGACGGAGGGAT	1104
RESULT 3			
US-10-082-828A-34			
; Sequence 34, Application US/10082828A			
; Publication No. US20030175715A1			
; GENERAL INFORMATION:			
; APPLICANT: Sun, Yongming			
; APPLICANT: Recipon, Herve			
; APPLICANT: Salceda, Susana			
; APPLICANT: Liu, Chenghua			
; APPLICANT: Turnez, Leah			
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr			
; FILE REFERENCE: DEX-0247			
; CURRENT APPLICATION NUMBER: US/10/082,828			
; PRIOR FILING DATE: 2002-07-09			
; PRIOR APPLICATION NUMBER: US 60/243,805			
; PRIOR FILING DATE: 2000-10-27			
; NUMBER OF SEQ ID NOS: 266			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 34			
; TYPE: DNA			
; LENGTH: 307			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc feature			
; LOCATION: (28)-(28)			
; OTHER INFORMATION: n=a, c, g or t			
US-10-082-828A-34			

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Query Match      47.9%; Score 306; DB 16; Length 307;
Best Local Similarity 99.7%; Pred. No. 9.3e-88;
Matches 306; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 333 GGTAAAGAGAAGCATCTGTATAGGAGGCAAGAGATCTGAGTCTCTTTTGAAGGCTATCTC 392
Db 1 GGTAAAGAGAAGCATCTGTATAGGAGGCAAGAGATCTGAGTCTCTTTTGAAGGCTATCTC 60

Qy 393 TGCTCTGTATCTCAATTAATCTGTTCTTCAATTTCAATTAATCTTACTACTATTCAGTTCCC 452
Db 61 TGCTCTGTATCTCAATTAATCTGTTCTTCAATTTCAATTAATCTTACTACTATTCAGTTCCC 120

Qy 453 TTGATCTTTTCTCTTGGGGCTGCTTAGGCTCAGGGAGATTCGAGAAGCACCAGAACT 512
Db 121 TTGATCTTTTCTCTTGGGGCTGCTTAGGCTCAGGGAGATTCGAGAAGCACCAGAACT 180

Qy 513 AGGAGCAGCCCTGAGACATGGGGAGTTCGAGCTGAAGCAGGAATGGCAGGATGAAGAATT 572
Db 181 AGGAGCAGCCCTGAGACATGGGGAGTTCGAGCTGAAGCAGGAATGGCAGGATGAAGAATT 240

Qy 573 CCCTAGGTGAGACCTGTGAGGCTGGCTGGGAGAAAGGAGGGTGGTCAAGAAATGGACGG 632
Db 241 CCCTAGGTGAGACCTGTGAGGCTGGCTGGGAGAAAGGAGGGTGGTCAAGAAATGGACGG 300

Qy 633 AGGGGAT 639
Db 301 AGGGGAT 307

RESULT 4
US-11-057-807-34
; Sequence 34, Application US/11057807
; Publication No. US20050136473A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Herve
; APPLICANT: Salceda, Susana
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and P
; FILE REFERENCE: DEX-0247
; CURRENT APPLICATION NUMBER: US/11/057,807
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US/10/082,828
; PRIOR FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/243,805
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28)..(28)
; OTHER INFORMATION: n=a, c, g or t
US-11-057-807-34

Query Match      47.9%; Score 306; DB 24; Length 307;
Best Local Similarity 99.7%; Pred. No. 9.3e-88;
Matches 306; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 333 GGTAAAGAGAAGCATCTGTATAGGAGGCAAGAGATCTGAGTCTCTTTTGAAGGCTATCTC 392
Db 1 GGTAAAGAGAAGCATCTGTATAGGAGGCAAGAGATCTGAGTCTCTTTTGAAGGCTATCTC 60

Qy 393 TGCTCTGTATCTCAATTAATCTGTTCTTCAATTTCAATTAATCTTACTACTATTCAGTTCCC 452
Db 61 TGCTCTGTATCTCAATTAATCTGTTCTTCAATTTCAATTAATCTTACTACTATTCAGTTCCC 120

Qy 453 TTGATCTTTTCTCTTGGGGCTGCTTAGGCTCAGGGAGATTCGAGAAGCACCAGAACT 512
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Db 121 TTGATCTTTTCTCTTGGGGCTGCTTAGGCTCAGGGAGATTCGAGAAGCACCAGAACT 180

Qy 513 AGGAGCAGCCCTGAGACATGGGGAGTTCGAGCTGAAGCAGGAATGGCAGGATGAAGAATT 572
Db 181 AGGAGCAGCCCTGAGACATGGGGAGTTCGAGCTGAAGCAGGAATGGCAGGATGAAGAATT 240

Qy 573 CCCTAGGTGAGACCTGTGAGGCTGGCTGGGAGAAAGGAGGGTGGTCAAGAAATGGACGG 632
Db 241 CCCTAGGTGAGACCTGTGAGGCTGGCTGGGAGAAAGGAGGGTGGTCAAGAAATGGACGG 300

Qy 633 AGGGGAT 639
Db 301 AGGGGAT 307

RESULT 5
US-10-104-047-1145
; Sequence 1145, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1145
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1145

Query Match      15.6%; Score 99.8; DB 17; Length 2112;
Best Local Similarity 89.9%; Pred. No. 8e-21;
Matches 107; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 477 TCTTAGGTCTAGGAGATTCGAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGA 536
Db 161 TGTGGGGTCTAGGAGATTCGAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGA 220

Qy 537 GTTGGAGCTGAAGAGGAATGGCAGGATGAAGAATTCCTAGTGAGGACGTTGTGAGG 595
Db 221 GTTGGAGCTGAAGAGGAATGGCAGGATGAAGAATTCCTAGTGAGGAGG 279

RESULT 6
US-10-198-846-13943/C
; Sequence 13943, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13943
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: 1, 500, 501, 502, 503
; OTHER INFORMATION: n = A,T,C or G
US-10-846-13943

Query Match      11.9%; Score 75.8; DB 14; Length 503;
Best Local Similarity 97.5%; Pred. No. 2.1e-13;
Matches 77; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 561 GGATGAAGAATTCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAAGGGGGTGGTC 620
Db 499 GGATGAAGAATTCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAAGGGGGTGGTC 440

Qy 621 ACGAATGACGAGGGGAT 639
Db 439 ACGAATGACGAGGGAT 421

RESULT 7
US-10-087-192-985
; Sequence 985, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 52945200122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 985
; LENGTH: 202251
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(202251)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-985

Query Match      7.1%; Score 45.2; DB 13; Length 202251;
Best Local Similarity 52.7%; Pred. No. 0.034;
Matches 98; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy 452 CTTGATCTTTTCTTCTTGGGGCTGCTTAGGGTCAGGAGATTGCGAAGACAGAAC 511
Db 140383 CCGACATTTGGACCTTGGGAGAGACAGAGATCAGTAGCAGCAGCAGCAG 140442

Qy 512 TAGGACAGCCCTGAGACATGGGGAGTTGGAGCTTGAAGGAGGAATGGCAGGATGAAGAAT 571
Db 140443 CAGCAGGAGAAAGAGGAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 140502

Qy 572 TCCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAAGGGAGGGTGGTCAGGAATGAGC 631
Db 140503 AAGGAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 140562

Qy 632 GAGGG 637
Db 140563 AAGAGG 140568

RESULT 8
US-09-904-968A-1/c
; Sequence 1, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMINO, Gregory

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; APPLICANT: WATNICK, Terry
; APPLICANT: PHAKDEKITCHARON, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
; FILE REFERENCE: JHU1680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 53522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-968A-1

Query Match      6.6%; Score 42; DB 10; Length 53522;
Best Local Similarity 52.9%; Pred. No. 0.18;
Matches 90; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

Qy 469 GGGGGCTGCTTAGGGTCAGGAGATTGCAGAGACACAGAACTTAGAGGAGCCCTGAGA 528
Db 34691 GGGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 34632

Qy 529 CATGGGGAGTTGGAGCTGAAGGAGGAATGCAGAGATGAAGAATCCCTAGGTGAGGACGT 588
Db 34631 GAGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 34572

Qy 589 GTGAGGTGCTGGGAGAAAGGAGGGGTGCTCAGCAATGCAGGAGGAGGAGGAGGAGGAG 638
Db 34571 GAGGGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 34522

RESULT 9
US-10-021-323-1875
; Sequence 1875, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 1875
; LENGTH: 540
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3825-006-Q1-N6-H8
US-10-021-323-1875

Query Match      6.1%; Score 39.2; DB 19; Length 540;
Best Local Similarity 47.2%; Pred. No. 0.14;
Matches 119; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

Qy 386 TATCCTCTGCTGTATCTCAATTACTGTTCTTCAATTTCTTCAATTTCTTCAATTTCTT 445
Db 19 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 78

Qy 446 AGTTCCTTGATCTTTCTTCTTGGGGCTGCTTAGGGTCAGGAGATTGCAGAACGAC 505
Db 79 TGTTATTTTGTGTTATTTTGTGTTATTTGTTATTTGTTATTTGTTATTTGTTGTTGTTGTT 138

Qy 506 CAGAACTAGGAGCAGCCCTCAGACATGGGGAGTTGGAGCTGAAGAGGAGGAATGGCAGGATG 565

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Db 139 TGGCAAGGGGGGGGGGGGGAGGGGGGGGGGGGGGGGGGGGGGGAGGGGGGGGGAGAGGGGGG 198
Qy 566 AAGAAATCCCTAGGTAGGACGTGTGAGGGTGGTGGGAGAGGGGGGGTGGTCAAGAA 625
Db 199 AAAAAAGGGGGGGGGGGGGAAAAAGGGGCAACCGGAGAGAGAAAAAGAGGGGAACAA 258
Qy 626 TGGACGGAGGGG 637
Db 259 AAAAAACAAAGG 270

RESULT 10

US-10-027-632-236295/c
; Sequence 236295, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236295
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(610)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-236295

Query Match 5.9%; Score 37.4; DB 13; Length 610;
Best Local Similarity 52.2%; Pred. No. 0.56;
Matches 83; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
Qy 309 AATCTGCTTCTAGCAAGTGGTGAAGTAAGAGAGCATCTGTATAGGAGGCAAGAGATCT 368
Db 565 AGTTTCCCTTTAGCCAAAGAGAGAGAAAAATGAATGCATAGAGATCCATGTAGATCA 506
Qy 369 GAGTCCTTTTGAAGGCCATCTCTGCTCTGTATCTCAATTACTGTTCTTCTTCAATT 428
Db 505 GTGGCTCTTGAATCTTTATCTTAAGATCTGTTCTCTCATCTTCTATGCTTCTATCCAC 446
Qy 429 ATTCTTACTACTATTCAGTTCCCTTGATCTTTTCTTCT 467
Db 445 AGTTGGCATCTTAAATTTTCCCAACTCCTATATTTAT 407

RESULT 11

US-10-027-632-236296/c
; Sequence 236296, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236296
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(610)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-236296
Query Match 5.9%; Score 37.4; DB 13; Length 610;
Best Local Similarity 52.2%; Pred. No. 0.56;
Matches 83; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
Qy 309 AATCTGCTTCTAGCAAGTGGTGAAGTAAGAGAGCATCTGTATAGGAGGCAAGAGATCT 368
Db 565 AGTTTCCCTTTAGCCAAAGAGAGAGAAAAATGAATGCATAGAGATCCATGTAGATCA 506
Qy 369 GAGTCCTTTTGAAGGCCATCTCTGCTCTGTATCTCAATTACTGTTCTTCTTCAATT 428
Db 505 GTGGCTCTTGAATCTTTATCTTAAGATCTGTTCTCTCATCTTCTATGCTTCTATCCAC 446
Qy 429 ATTCTTACTACTATTCAGTTCCCTTGATCTTTTCTTCT 467
Db 445 AGTTGGCATCTTAAATTTTCCCAACTCCTATATTTAT 407

RESULT 12

US-10-027-632-236297/c
; Sequence 236297, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720

; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236295
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(610)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-236295

Query Match 5.9%; Score 37.4; DB 17; Length 610;
Best Local Similarity 52.2%; Pred. No. 0.56;
Matches 83; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
Qy 309 AATCTGCTTCTAGCAAGTGGTAAGAGAGCAATCTGTATAGGAGGCAAGAGATCT 368
Db 565 AGTTTCCCTTTAGCCAGGAAGAGAAAAAATGAATGCATAGAGATCCCATGTAGATCA 506
Qy 369 GAGTCCTTTTGAAGCCCTATCCTCTGCTCTGTATCTCAATTACTGTCTTCTTCAATT 428
Db 505 GTGGCTCTTGAATTCCTTTATCCTAAGATCTGTTTCTCTCATTCATCTCTTATCCAC 446
Qy 429 ATTCTTACTACTATTTCAGTTCCCTTGATCTTTTCTTCT 467
Db 445 AGTTTGGCATCTTAAATTTTCCCACTCCTATATTAT 407

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Job time : 2054 secs

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